SEQUENCE LISTING

B1

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<120> TRANSFORMED MICROORGANISMS WITH IMPROVED PROPERTIES

<130> 0933-148P

<140> 09/423,554
<141> 1999-11-10

<150> PCT/FI99/00185
<151> 1999-03-11

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<170> PatentIn Ver. 2.0

<210> 1
<211> 71
<212> PRT
<213> Aspergillus nidulans

<400> 1

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Leu Arg Gln Arg Arg Ala Gln Gly Glu Glu Tyr Asp Lys Phe Val Asp
             20                  25                  30

Lys Phe Val Arg Met Ala Gly Arg Gly Phe Pro Met Pro Ile Ser Thr
         35                  40                  45

Cys Ser Glu Asp Phe Gly Leu Gln Asn Ala Lys Arg Ile Leu Asp Arg
     50                  55                  60

Tyr Arg Ser Gln Leu Pro Cys
 65                  70
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<210> 2

B1

<211> 156
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<213> Trichoderma reesei

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Gly Cys Arg Asn Ser Ala Arg Gly Met Asn Ser Ile Leu Arg Thr Thr
             20                  25                  30

Ser Ser Arg Leu Ser Lys Ser Ser Asn Ile His Cys Thr Ser Thr Leu
         35                  40                  45

Arg Tyr Ser Pro Gln Arg Ser Ser Ser Pro Leu Cys Cys Lys Pro Arg
     50                  55                  60

Ser Ser Ser Ser Leu Thr Met Ser Ser Ser Lys Pro Thr Lys Phe Ser
 65                  70                  75                  80

His Leu Pro Leu Ser Thr Thr Gly Pro Leu Glu Cys Ala Leu Thr Gly
                 85                  90                  95

Thr Ala Leu Leu Asn Ser Pro Ile Phe Asn Lys Gly Ser Ala Phe Pro
            100                 105                 110

Leu Ser Glu Arg Arg Gln Phe Asn Leu Thr Gly Leu Leu Pro Ala Asn
        115                 120                 125

Glu Gln Thr Leu Asp Asn Gln Val Lys Arg Ala Tyr Gln Gln Tyr Gln
    130                 135                 140

Ser Arg Gly Asp Asp Trp Pro Arg Thr Val Pro Asp
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<210> 3
<211> 584
<212> PRT
<213> Homo sapiens

<400> 3

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Arg His Leu His Ile Lys Glu Lys Gly Lys Pro Leu Met Leu Asn Pro
             20                  25                  30
```

Arg Thr Asn Lys Gly Met Ala Phe Thr Leu Gln Glu Arg Gln Met Leu
35 40 45

Gly Leu Gln Gly Leu Leu Pro Pro Lys Ile Glu Thr Gln Asp Ile Gln
50 55 60

Ala Leu Arg Phe His Arg Asn Leu Lys Lys Met Thr Ser Pro Leu Glu
65 70 75 80

Lys Tyr Ile Tyr Ile Met Gly Ile Gln Glu Arg Asn Glu Lys Leu Phe
85 90 95

Tyr Arg Ile Leu Gln Asp Asp Ile Glu Ser Leu Met Pro Ile Val Tyr
100 105 110

Thr Pro Thr Val Gly Leu Ala Cys Ser Gln Tyr Gly His Ile Phe Arg
115 120 125

Arg Pro Lys Gly Leu Phe Ile Ser Ile Ser Asp Arg Gly His Val Arg
130 135 140

Ser Ile Val Asp Asn Trp Pro Glu Asn His Val Lys Ala Val Val Val
145 150 155 160

Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly Asp Leu Gly Val Tyr Gly
165 170 175

Met Gly Ile Pro Val Gly Lys Leu Cys Leu Tyr Thr Ala Cys Ala Gly
180 185 190

Ile Arg Pro Asp Arg Cys Leu Pro Val Cys Ile Asp Val Gly Thr Asp
195 200 205

Asn Ile Ala Leu Leu Lys Asp Pro Phe Tyr Met Gly Leu Tyr Gln Lys
210 215 220

Arg Asp Arg Thr Gln Gln Tyr Asp Asp Leu Ile Asp Glu Phe Met Lys
225 230 235 240

Ala Ile Thr Asp Arg Tyr Gly Arg Asn Thr Leu Ile Gln Phe Glu Asp
245 250 255

Phe Gly Asn His Asn Ala Phe Arg Phe Leu Arg Lys Tyr Arg Glu Lys
260 265 270

Tyr Cys Thr Phe Asn Asp Asp Ile Gln Gly Thr Ala Ala Val Ala Leu
275 280 285

[redacted]

B'

```
Ala Gly Leu Leu Ala Ala Gln Lys Val Ile Ser Lys Pro Ile Ser Glu
    290                 295                 300

His Lys Ile Leu Phe Leu Gly Ala Gly Glu Ala Ala Leu Gly Ile Ala
305                 310                 315                 320

Asn Leu Ile Val Met Ser Met Val Glu Asn Gly Leu Ser Glu Gln Glu
                325                 330                 335

Ala Gln Lys Lys Ile Trp Met Phe Asp Lys Tyr Gly Leu Leu Val Lys
            340                 345                 350

Gly Arg Lys Ala Lys Ile Asp Ser Tyr Gln Glu Pro Phe Thr His Ser
        355                 360                 365

Ala Pro Glu Ser Ile Pro Asp Thr Phe Glu Asp Ala Val Asn Ile Leu
    370                 375                 380

Lys Pro Ser Thr Ile Ile Gly Val Ala Gly Ala Gly Arg Leu Phe Thr
385                 390                 395                 400

Pro Asp Val Ile Arg Ala Met Ala Ser Ile Asn Glu Arg Pro Val Ile
                405                 410                 415

Phe Ala Leu Ser Asn Pro Thr Ala Gln Ala Glu Cys Thr Ala Glu Glu
            420                 425                 430

Ala Tyr Thr Leu Thr Glu Gly Arg Cys Leu Phe Ala Ser Gly Ser Pro
        435                 440                 445

Phe Gly Pro Val Lys Leu Thr Asp Gly Arg Val Phe Thr Pro Gly Gln
    450                 455                 460

Gly Asn Asn Val Tyr Ile Phe Pro Gly Val Ala Leu Ala Val Ile Leu
465                 470                 475                 480

Cys Asn Thr Arg His Ile Ser Asp Ser Val Phe Leu Glu Ala Ala Lys
                485                 490                 495

Ala Leu Thr Ser Gln Leu Thr Asp Glu Glu Leu Ala Gln Gly Arg Leu
            500                 505                 510

Tyr Pro Pro Leu Ala Asn Ile Gln Glu Val Ser Ile Asn Ile Ala Ile
        515                 520                 525

Lys Val Thr Glu Tyr Leu Tyr Ala Asn Lys Met Ala Phe Arg Tyr Pro
    530                 535                 540
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B'

```
Glu Pro Glu Asp Lys Ala Lys Tyr Val Lys Glu Arg Thr Trp Arg Ser
545                 550                 555                 560

Glu Tyr Asp Ser Leu Leu Pro Asp Val Tyr Glu Trp Pro Glu Ser Ala
                565                 570                 575

Ser Ser Pro Pro Val Ile Thr Glu
            580
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<210> 4
<211> 565
<212> PRT
<213> Schizosaccharomyces pombe

<400> 4

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Thr Leu Leu Asn Ser Pro Arg Tyr Asn Lys Asp Thr Ala Phe Thr Pro
             20                  25                  30

Glu Glu Arg Gln Lys Phe Glu Ile Ser Ser Arg Leu Pro Pro Ile Val
         35                  40                  45

Glu Thr Leu Gln Gln Gln Val Asp Arg Cys Tyr Asp Gln Tyr Lys Ala
     50                  55                  60

Ile Gly Asp Glu Pro Leu Gln Lys Asn Leu Tyr Leu Ser Gln Leu Ser
 65                  70                  75                  80

Val Thr Asn Gln Thr Leu Phe Tyr Ala Leu Ile Ser Gln His Leu Ile
                 85                  90                  95

Glu Met Ile Pro Ile Ile Tyr Thr Pro Thr Glu Gly Asp Ala Ile Lys
            100                 105                 110

Gln Phe Ser Asp Ile Tyr Arg Tyr Pro Glu Gly Cys Tyr Leu Asp Ile
        115                 120                 125

Asp His Asn Asp Leu Ser Tyr Ile Lys Gln Gln Leu Ser Glu Phe Gly
    130                 135                 140

Lys Ser Asp Ser Val Glu Tyr Ile Ile Ile Thr Asp Ser Glu Gly Ile
145                 150                 155                 160

Leu Gly Ile Gly Asp Gln Gly Val Gly Gly Val Leu Ile Ser Val Ala
                165                 170                 175
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Lys Gly His Leu Met Thr Leu Cys Ala Gly Leu Asp Pro Asn Arg Phe
180 185 190

Leu Pro Ile Val Leu Asp Val Gly Thr Asn Asn Glu Thr His Arg Lys
195 200 205

Asn His Gln Tyr Met Gly Leu Arg Lys Asp Arg Val Arg Gly Glu Gln
210 215 220

Tyr Asp Ser Phe Leu Asp Asn Val Ile Lys Ala Ile Arg Glu Val Phe
225 230 235 240

Pro Glu Ala Phe Ile His Phe Glu Asp Phe Gly Leu Ala Asn Ala Lys
245 250 255

Arg Ile Leu Asp His Tyr Arg Pro Asp Ile Ala Cys Phe Asn Asp Asp
260 265 270

Ile Gln Gly Thr Gly Ala Val Ala Leu Ala Ala Ile Ile Gly Ala Leu
275 280 285

His Val Thr Lys Ser Pro Leu Thr Glu Gln Arg Ile Met Ile Phe Gly
290 295 300

Ala Gly Thr Ala Gly Val Gly Ile Ala Asn Gln Ile Val Ala Gly Met
305 310 315 320

Val Thr Asp Gly Leu Ser Leu Asp Lys Ala Arg Gly Asn Leu Phe Met
325 330 335

Ile Asp Arg Cys Gly Leu Leu Leu Glu Arg His Ala Lys Ile Ala Thr
340 345 350

Asp Gly Gln Lys Pro Phe Leu Lys Lys Asp Ser Asp Phe Lys Glu Val
355 360 365

Pro Ser Gly Asp Ile Asn Leu Glu Ser Ala Ile Ala Leu Val Lys Pro
370 375 380

Thr Ile Leu Leu Gly Cys Ser Gly Gln Pro Gly Lys Phe Thr Glu Lys
385 390 395 400

Ala Ile Arg Glu Met Ser Lys His Val Glu Arg Pro Ile Ile Phe Pro
405 410 415

Ile Ser Asn Pro Thr Thr Leu Met Glu Ala Lys Pro Asp Gln Ile Asp
420 425 430

[redacted]

B1

```
Lys Trp Ser Asp Gly Lys Ala Leu Ile Ala Thr Gly Ser Pro Leu Pro
        435                 440                 445

Pro Leu Asn Arg Asn Gly Lys Lys Tyr Val Ile Ser Gln Cys Asn Asn
    450                 455                 460

Ala Leu Leu Tyr Pro Ala Leu Gly Val Ala Cys Val Leu Ser Arg Cys
465                 470                 475                 480

Lys Leu Leu Ser Asp Gly Met Leu Lys Ala Ala Ser Asp Ala Leu Ala
                485                 490                 495

Thr Val Pro Arg Ser Leu Phe Ala Ala Asp Glu Ala Leu Leu Pro Asp
            500                 505                 510

Leu Asn Asn Ala Arg Glu Ile Ser Arg His Ile Val Phe Ala Val Leu
        515                 520                 525

Lys Gln Ala Val Ser Glu Gly Met Ser Thr Val Asp Leu Pro Lys Asp
    530                 535                 540

Asp Ala Lys Leu Lys Glu Trp Ile Ile Glu Arg Glu Trp Asn Pro Glu
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Tyr Lys Pro Phe Val
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<211> 669
<212> PRT
<213> Saccharomyces cerevisiae

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Thr Arg Ser Leu Thr Ala Ser Arg Thr Ala Pro Leu Arg Arg Trp Pro
             20                  25                  30

Ile Gln Gln Ser Arg Leu Tyr Ser Ser Asn Thr Arg Ser His Lys Ala
         35                  40                  45

Thr Thr Thr Arg Glu Asn Thr Phe Gln Lys Pro Tyr Ser Asp Glu Glu
     50                  55                  60

Val Thr Lys Thr Pro Val Gly Ser Arg Ala Arg Lys Ile Phe Glu Ala
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```
 65                  70                  75                  80

Pro His Pro His Ala Thr Arg Leu Thr Val Glu Gly Ala Ile Glu Cys
                 85                  90                  95

Pro Leu Glu Ser Phe Gln Leu Leu Asn Ser Pro Leu Phe Asn Lys Gly
            100                 105                 110

Ser Ala Phe Thr Gln Glu Glu Arg Glu Ala Phe Asn Leu Glu Ala Leu
        115                 120                 125

Leu Pro Pro Gln Val Asn Thr Leu Asp Glu Gln Leu Glu Arg Ser Tyr
    130                 135                 140

Lys Gln Leu Cys Tyr Leu Lys Thr Pro Leu Ala Lys Asn Asp Phe Met
145                 150                 155                 160

Thr Ser Leu Arg Val Gln Asn Lys Val Leu Tyr Phe Ala Leu Ile Arg
                165                 170                 175

Arg His Ile Lys Glu Leu Val Pro Ile Ile Tyr Thr Pro Thr Glu Gly
            180                 185                 190

Asp Ala Ile Ala Ala Tyr Ser His Arg Phe Arg Lys Pro Glu Gly Val
        195                 200                 205

Phe Leu Asp Ile Thr Glu Pro Asp Ser Ile Glu Cys Arg Leu Ala Thr
    210                 215                 220

Tyr Gly Gly Asp Lys Asp Val Asp Tyr Ile Val Val Ser Asp Ser Glu
225                 230                 235                 240

Gly Ile Leu Gly Ile Gly Asp Gln Gly Ile Gly Gly Val Arg Ile Ala
                245                 250                 255

Ile Ser Lys Leu Ala Leu Met Thr Leu Cys Gly Gly Ile His Pro Gly
            260                 265                 270

Arg Val Leu Pro Val Cys Leu Asp Val Gly Thr Asn Asn Lys Lys Leu
        275                 280                 285

Ala Arg Asp Glu Leu Tyr Met Gly Asn Lys Phe Ser Arg Ile Arg Gly
    290                 295                 300

Lys Gln Tyr Asp Asp Phe Leu Glu Lys Phe Ile Lys Ala Val Lys Lys
305                 310                 315                 320

Val Tyr Pro Ser Ala Val Leu His Phe Glu Asp Phe Gly Val Lys Asn
```

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```
                325                 330                 335

Ala Arg Arg Leu Leu Glu Lys Tyr Arg Tyr Glu Leu Pro Ser Phe Asn
            340                 345                 350

Asp Asp Ile Gln Gly Thr Gly Ala Val Val Met Ala Ser Leu Ile Ala
        355                 360                 365

Ala Leu Lys His Thr Asn Arg Asp Leu Lys Asp Thr Arg Val Leu Ile
    370                 375                 380

Tyr Gly Ala Gly Ser Ala Gly Leu Gly Ile Ala Asp Gln Ile Val Asn
385                 390                 395                 400

His Met Val Thr His Gly Val Asp Lys Glu Glu Ala Arg Lys Lys Ile
                405                 410                 415

Phe Leu Met Asp Arg Arg Gly Leu Ile Leu Gln Ser Tyr Glu Ala Asn
            420                 425                 430

Ser Thr Pro Ala Gln His Val Tyr Ala Lys Ser Asp Ala Glu Trp Ala
        435                 440                 445

Gly Ile Asn Thr Arg Ser Leu His Asp Val Val Glu Asn Val Lys Pro
    450                 455                 460

Thr Cys Leu Val Gly Cys Ser Thr Gln Ala Gly Ala Phe Thr Gln Asp
465                 470                 475                 480

Val Val Glu Glu Met His Lys His Asn Pro Arg Pro Ile Ile Phe Pro
                485                 490                 495

Leu Ser Asn Pro Thr Arg Leu His Glu Ala Val Pro Ala Asp Leu Met
            500                 505                 510

Lys Trp Thr Asn Asn Asn Ala Leu Val Ala Thr Gly Ser Pro Phe Pro
        515                 520                 525

Pro Val Asp Gly Tyr Arg Ile Ser Glu Asn Asn Asn Cys Tyr Ser Phe
    530                 535                 540

Pro Gly Ile Gly Leu Gly Ala Val Leu Ser Arg Ala Thr Thr Ile Thr
545                 550                 555                 560

Asp Lys Met Ile Ser Ala Ala Val Asp Gln Leu Ala Glu Leu Ser Pro
                565                 570                 575

Leu Arg Glu Gly Asp Ser Arg Pro Gly Leu Leu Pro Gly Leu Asp Thr
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580 585 590

Ile Thr Asn Thr Ser Ala Arg Leu Ala Thr Ala Val Ile Leu Gln Ala
595 600 605

Leu Glu Glu Gly Thr Ala Arg Ile Glu Gln Glu Gln Val Pro Gly Gly
610 615 620

Ala Pro Gly Glu Thr Val Lys Val Pro Arg Asp Phe Asp Glu Cys Leu
625 630 635 640

Gln Trp Val Lys Ala Gln Met Trp Glu Pro Val Tyr Arg Pro Met Ile
645 650 655

Lys Val Gln His Asp Pro Ser Val His Thr Asn Gln Leu
660 665

<210> 6
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 6
ccagtgatat cgaggatgag attagtac 28

<210> 7
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 7
ccagtgatat ctgtacttgt cagggcat 28

<210> 8
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 8
catgctaagc ttctagaatg cttagaacca gacta 35

<210> 9
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 9
gatgctaagc ttctagatgg ttatgcttcg tctac 35

<210> 10
<211> 17
<212> PRT
<213> Aspergillus nidulans

<400> 10
Phe Asn Asp Asp Ile Gln Gly Thr Gly Ala Val Val Met Ala Ser Leu
1 5 10 15

Ile

<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

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<222> (1)..(17)
<223> Any N = Inosine

<400> 11
gaygtnggna cnaayaa 17

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
<221> modified_base
<222> (1)..(23)
<223> N = Inosine

<400> 12
gtnccytgda trtcrtcrtt raa 23

<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 13
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<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 14
caggatcctc tgttagggat ttactcc 27

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Receipt

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First Named Inventor:	Aristos ARISTIDOU
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